

OM protein - protein search, using sw model

Run on: January 23, 2006, 07:58:20 ; Search time 134 Seconds
(without alignments)
295.105 Million cell updates/sec

Title: US-10-820-136-2
Perfect score: 451
Sequence: 1 MRLSVCLLMVSLALCCYQAH.....FKKRLSLEKVLVEIVKKCGV 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

OM protein - protein search, using sw model

Run on: January 23, 2006, 08:09:55 ; Search time 39 Seconds
(without alignments)
222.039 Million cell updates/sec

Title: US-10-820-136-2
Perfect score: 451
Sequence: 1 MRLSVCLLMVSLALCCYQAH.....FKKRLSLEKVLVEIVKKCGV 90


Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%



Maximum Match 100%
Listing first 100 summaries

Database :

PIR_80:*
1: pirl1:*
2: pir2:*
3: pir3:*
4: pir4:*

OM protein - protein search, using sw model

Run on: January 23, 2006, 08:12:50 ; Search time 45 Seconds
(without alignments)
165.351 Million cell updates/sec

Title: US-10-820-136-2
Perfect score: 451
Sequence: 1 MRLSVCLLMVSLALCCYQAH.....FKKRLSLEKVLVEIVKKCGV 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

OM protein - protein search, using sw model

Run on: January 23, 2006, 08:18:56 ; Search time 116 Seconds
(without alignments)
324.178 Million cell updates/sec

Title: US-10-820-136-2
Perfect score: 451
Sequence: 1 MRLSVCLLMVSLALCCYQAH.....FKKRLSLEKVLVEIVKKCGV 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

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OM protein - protein search, using sw model

Run on: January 23, 2006, 08:19:42 ; Search time 30 Seconds
(without alignments)
30.402 Million cell updates/sec

Title: US-10-820-136-2
Perfect score: 451
Sequence: 1 MRLSVCLLMVSLALCCYQAH.....FKKRLSLEKVLVEIVKKCGV 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 70606

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

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OM protein - protein search, using sw model

Run on: January 23, 2006, 08:13:41 ; Search time 395 Seconds
(without alignments)
314.876 Million cell updates/sec

Title: US-10-820-136-2
Perfect score: 451
Sequence: 1 MRLSVCLLMVSLALCCYQAH.....FKKRLSLEKVLVEIVKKCGV 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 7861189 seqs, 1381955077 residues

Total number of hits satisfying chosen parameters: 7861189

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Pending_Patents_AA_Main:*

- 1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*
- 2: /cgn2_6/ptodata/1/paa/US066_COMB.pep:*
- 3: /cgn2_6/ptodata/1/paa/US073_COMB.pep:*
- 4: /cgn2_6/ptodata/1/paa/US074_COMB.pep:*
- 5: /cgn2_6/ptodata/1/paa/US075_COMB.pep:*
- 6: /cgn2_6/ptodata/1/paa/US076_COMB.pep:*
- 7: /cgn2_6/ptodata/1/paa/US077_COMB.pep:*
- 8: /cgn2_6/ptodata/1/paa/US078_COMB.pep:*
- 9: /cgn2_6/ptodata/1/paa/US079_COMB.pep:*
- 10: /cgn2_6/ptodata/1/paa/US080_COMB.pep:*
- 11: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
- 12: /cgn2_6/ptodata/1/paa/US082_COMB.pep:*
- 13: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*
- 14: /cgn2_6/ptodata/1/paa/US084_COMB.pep:*
- 15: /cgn2_6/ptodata/1/paa/US085_COMB.pep:*
- 16: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*
- 17: /cgn2_6/ptodata/1/paa/US087_COMB.pep:*
- 18: /cgn2_6/ptodata/1/paa/US088_COMB.pep:*
- 19: /cgn2_6/ptodata/1/paa/US089_COMB.pep:*
- 20: /cgn2_6/ptodata/1/paa/US090_COMB.pep:*
- 21: /cgn2_6/ptodata/1/paa/US091_COMB.pep:*
- 22: /cgn2_6/ptodata/1/paa/US092_COMB.pep:*
- 23: /cgn2_6/ptodata/1/paa/US093_COMB.pep:*
- 24: /cgn2_6/ptodata/1/paa/US094_COMB.pep:*
- 25: /cgn2_6/ptodata/1/paa/US095_COMB.pep:*
- 26: /cgn2_6/ptodata/1/paa/US096_COMB.pep:*
- 27: /cgn2_6/ptodata/1/paa/US097_COMB.pep:*
- 28: /cgn2_6/ptodata/1/paa/US098_COMB.pep:*
- 29: /cgn2_6/ptodata/1/paa/US099_COMB.pep:*
- 30: /cgn2_6/ptodata/1/paa/US100_COMB.pep:*
- 31: /cgn2_6/ptodata/1/paa/US101_COMB.pep:*
- 32: /cgn2_6/ptodata/1/paa/US102_COMB.pep:*
- 33: /cgn2_6/ptodata/1/paa/US103_COMB.pep:*
- 34: /cgn2_6/ptodata/1/paa/US104_COMB.pep:*
- 35: /cgn2_6/ptodata/1/paa/US105_COMB.pep:*
- 36: /cgn2_6/ptodata/1/paa/US106_COMB.pep:*
- 37: /cgn2_6/ptodata/1/paa/US107_COMB.pep:*
- 38: /cgn2_6/ptodata/1/paa/US108_COMB.pep:*
- 39: /cgn2_6/ptodata/1/paa/US109_COMB.pep:*
- 40: /cgn2_6/ptodata/1/paa/US110_COMB.pep:*
- 41: /cgn2_6/ptodata/1/paa/US111_COMB.pep:*
- 42: /cgn2_6/ptodata/1/paa/US112_COMB.pep:*
- 43: /cgn2_6/ptodata/1/paa/US114_COMB.pep:*
- 44: /cgn2_6/ptodata/1/paa/US600_COMB.pep:*
- 45: /cgn2_6/ptodata/1/paa/US601_COMB.pep:*
- 46: /cgn2_6/ptodata/1/paa/US602_COMB.pep:*
- 47: /cgn2_6/ptodata/1/paa/US603_COMB.pep:*
- 48: /cgn2_6/ptodata/1/paa/US604_COMB.pep:*
- 49: /cgn2_6/ptodata/1/paa/US605_COMB.pep:*
- 50: /cgn2_6/ptodata/1/paa/US606_COMB.pep:*
- 51: /cgn2_6/ptodata/1/paa/US607_COMB.pep:*

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OM protein - protein search, using sw model

Run on: January 23, 2006, 08:16:01 ; Search time 49 Seconds
(without alignments)
81.761 Million cell updates/sec

Title: \ US-10-820-136-2
Perfect score: 451
Sequence: 1 MRLSVCLLMVSLALCCYQAH.....FKKRLSLEKVLVEIVKKCGV 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174783 seqs, 44514105 residues

Total number of hits satisfying chosen parameters: 174783

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*